

Db 692 KERISAQKAEPPORPASEPHVYVAVKPRVIAQPSETHIKTKDQGNHISSOIKKTTDL 751
 QY 579 --EGVLVNHNEPRSSRIGLVRHF-----NLPEDDKGSEASSEAGVVTTRQ----- 622
 Db 752 TTERLVHVDKRPRTAS-----PHFTVSKISVPKTEHGYEASIAQSAIATLQKLSATSSA 806
 QY 623 -----TRPDSKOERENGQAKTPSPFVKPEPPVLAKP-----KLUS 660
 Db 807 OKIKSVKAPVYKPTRV-----AEPTLPQFPADPTDYTKSEAGVVKVKGVSING 862
 QY 661 TOLQOLINQV--LEOHQOLNPPSPKPEFPFMTVLNSNAPPATVTSXKOVKAPSSQTF 718
 Db 863 TVVREERFELHGREAKVTETARVAPVEIPV-----TPPTLVSLGNVTVIEGESV 914
 QY 719 SLARPKYFFSTNTT----- 733
 Db 915 TLECHISGYSPVTWYREDYQIESSIDFQTSQGIARLMIREAFADSGRSTCSAVNE 974
 QY 734 AATVAPSS-----SPVFLSSTPOTIQRTVSKESLLVSHPSVOTKSPGGLSTQNEPLPP 787
 Db 975 ACTVSTCYLAVOVSEEFKETTAVTEKFTTEKRFVESRDVMDT-----SLTEE--QA 1028
 QY 788 CPTETPPPP-----TFSPGNOFQPCV---SPIVPSPTSR----- 822
 Db 1029 GPGEPAAPIYITKPVVOKLVGGGVFCQVGNPKPHVYWKSGVPLTGYRYKVSYNK 1088
 QY 823 -----IONVAFSLSSVLPSPALPPTNAMXLPSPASPMPSOG 859
 Db 1089 QTGCKLVISMTFADGAGVTVVRNKHGCTSA---SASLLEADYELLAKSOEMLXQ- 1144
 QY 860 LAKNKTSPQVNDNIRET-----KNVIR-DLGKKTSDVRPNQOY 903
 Db 1145 -----TOTVAFVQEPVGTAGCFVSYEYKEQALIRKNAKTVVVRVYVEDQEF 1199
 QY 904 KISSEORLANEIEFLRTP-----VDESDDIOHDEIPTCKCIAPIFDKRLKHFRTG 959
 Db 1200 HISSFERLKEIEYRIKTLLEELLEDGEEKMAVDISEASEVESGFLRIKNYRILEG 1259
 QY 960 SPVFTCKIVGIPVYVWFKDGKQIKRNECHKRRREGQCTSLHISTTSDDDNYTI 1019
 Db 1260 MGVTFCMKSGYPLPKIANYKDGKRI-KHGERYQNDFLQDGRASLRIPVLPDEGIYTA 1318
 QY 1020 MAANPOGRICSGHLAVQ-----SL-----PIR----- 1042
 Db 1319 FASNIKNAICSGKLYVEPAALGAPTIIPILEPVSRISLSPRSVSRSPIRMSP 1378
 QY 1043 SRLTSACQSHGRS-----RVQERDKEPLQERFRPHFTLOAPGDMVAHEGRCLRDCKVSL 1099
 Db 1379 ARMSPARMSPARMSPGRRLEETDESQ-ERLYKPVFLKPVSEKLEGANCRCFLKVVGR 1437
 QY 1100 PPELTWLLNGQVLPDPASHRLMVBRETGVHSLLDPLTQRDAGTYKCIATNKTGQNSFSL 1159
 Db 1438 PMPETFHFDGQOIVNDYTHKVVIKEDTQSLIIVPATPSDSGEMTVVAGNRAGRSSISV 1497
 QY 1160 ELSVVAKEVKAPVILEKQNGVPEGHVBLEGRVIGMPPVYFKKKNETI-PCTRR 1218
 Db 1498 ILTVEAVEHVKPMFVEKLNKYNIEGSRLENKVRATGNPNFDVLKNSDIIVPHKYPK 1557
 QY 1219 ISKHODTGTACLLIOPAKSDAGWYLTUSAKNEAGVSCVSTARLOIYAQWHQIOPPMYSR 1278
 Db 1558 IRI-EGTKGEAALKIDSTVSODSANYTATAINAGROTTCKVNVVEFAEAPERKLII 1616
 QY 1279 PGS 1282
 Db 1617 PRGT 1620

RESULT 4

T29757

Protein UNC-89 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999

C:Accession: T29757

R:Du, Z.; Le, T.T.; Wilson, R.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid C09D1.
 A:Reference number: 220679
 A:Accession: T29757
 A:Status: Preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 16642 <DU2>
 A:Cross-references: EMBL:AF003131; PIDN:AA854132.1; GSPDB:GN00019; CESP:unc-89
 A:Experimental source: strain Bristol N2; clone C09D1
 C:Genetics:
 A:Gene: CESP:unc-89
 A:Map position: 1
 A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1
 /3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 8.88; Score 608; DB 2; Length 6642;
 Best Local Similarity 23.18; Pred. No. 4.3e-21;
 Matches 265; Conservative 160; Mismatches 468; Indels 252; Gaps 39;

QY 264 PLQPPRFTQKLSREVPEGARVQVDCIVVGIPIPPQVVRWYCEGKELENS----- 312
 Db 2749 PRCEPDPFLEMLSNVRARTGTAKVHKVVETGDKPKSLTWYNNKELNSDLTYIVTDOKT 2808
 QY 313 -----PDHIYOAGNLHSLTAEAFEDTGRVSCFASNIYGTDSIAEYIEG--- 360
 Db 2809 STLTINSFNPDVHGE-----IICK-ENGAGEVSCITANMITYTSDMFSESEAEAE 2860
 QY 361 --VSSSDSGDPPKEMNR-----TOKPNEVSSPTTSNAVTPPAVPAQ- 402
 Db 2861 EFVGDDLTDESLREEMHRTPTPYMAPKFIITKDKAKKGSAAVEFCVVPDTKGVCCCK 2920
 QY 403 -----HLVAOPRYAT-----IQ-----CQSPTN 421
 Db 2921 LKDGKEILIAIRVQTRTGEGHITQELVDNVTEDAGKYTCIVENTAGKDTCEATLT 2980
 QY 422 YLQGLDGKPLIAAPVTRKMLNLSAGOLVVFECRVKAGSPKVKMYEGTLIEDSPDF 481
 Db 2981 VIESLEKKSEKKAPEFIVALODKTKTSEKVLCEKVICPRPKVSWLHDNVSREKNNS 3040
 QY 482 -RLQKKPRMAEPEICTLVIAEVAEDSGCCTCTASNKTKTVSSIAQLHVRG----- 534
 Db 3041 EKTITQESITVESVGERVTTITSELSHOCKYTCIAENTEGSKTEAFLTVQGEAPVFT 3100
 QY 535 ----NEDLSNNSLSHANSSTNLAAIEPQSPHSPSPSPVQPPAPKLEGVLVNHNEPRS 590
 Db 3101 KELQNKELSIGEKLVLSGVK-----SPQ---PHVDYFSEETKVE-----TKITS 3145
 QY 591 SSRIGLVRHFNLPEDDKGSEASEAGVVTTRQTRPD-----SXOERFNCQATKTPSPFP 645
 Db 3146 SSRIAI-----EHD---QNTNHRVVISQITKEDIVSKATNSIGTANSTSKITK 3195
 QY 646 VKEPPVLAKPKLDSTOLOQLHNOVLLEQHLQLOPPSPSPKPEFPFMTVLNSNAPPVTT 705
 Db 3196 VEAP---VFEQGLKTSYKE-----KEEKMEKVGGSAPDVEM---FKDDKPVSEDG 3242
 QY 706 SXKOVKAPSSQTFSLARPKYFPFTNTTAATVAPSSPVFTLSST-----PQTIQRTYSR 760
 Db 3243 NHMKKNPETGVFTLVWQK---AATDAGKYTAKASNPACTAESAEAEVTSLEKPTFV 3299
 QY 761 ESSLVSHPSVQTKSPGGLSIGNED-----LPQPEPTPPPTFESIPSGNQFQPCVSP 818
 Db 3300 RELVTEYKINETATLSVTVKGVDPSPVEMKQGVQVQDSSHVIAKVEGSGSYITND 3359
 QY 815 IPVSPS-----RIQNPVAFIS-----SVLPSLPAIPTTNAMXL-PRSAFSPMSQGLAKN 864
 Db 3360 ARLEDGKYACRATNPAGEAKTEANFAVWNL--VPEFVEKLPSPLEVKEKESTTSLVKV 3417
 QY 865 TKSPQ-----PVNDDNIR--ETKNVIRDLGK-KITESDVRPNQOQYKISSFQR 911
 Db 3418 VGTPEPSVEMFKDDTPISIDNVHVIRQTAV---GSFSLTINDARQGD---VGIYSR 3469
 QY 912 LWNTEFLRTPVDESDEIQHDEIFTGCIAPIDFKRLKHFRTGSPVFTTCTGIVGI 971